

ADM72285
 ID ADM72285 standard; protein; 1030 AA.
 XX
 AC ADM72285;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Porcine TLR9 polypeptide.
 XX
 KW TLR9; toll-like receptor 9; CpG; TLR9 signaling; porcine.
 XX
 OS Sus scrofa.
 XX
 PN WO2004026888-A2.
 XX
 PD 01-APR-2004.
 XX
 PF 19-SEP-2003; 2003WO-US029577.
 XX
 PR 19-SEP-2002; 2002US-0412479P.
 XX
 PA (COLE-) COLEY PHARM GMBH.
 PA (UYSA-) UNIV SASKATCHEWAN.
 PA (QIAG-) QIAGEN GMBH.
 XX
 PI Lipford GB, Mookherjee N, Babiuk L, Brownlie R, Griebel P;
 PI Mutwiri G, Hecker R;
 XX
 DR WPI; 2004-295374/27.
 DR N-PSDB; ADM72287.
 XX
 PT New polypeptide, useful for identifying key amino acids in a TLR9 of a
 PT first species which confer specificity for CpG DNA optimized for TLR9 of
 PT the first species.
 XX
 PS Claim 1; SEQ ID NO 5; 170pp; English.
 XX
 CC The invention relates to novel Toll-like receptor 9 (TLR9) polypeptides
 CC and encoding polynucleotides. It provides methods for (i) identifying key
 CC amino acids in a TLR9 of a first species which confer specificity for CpG
 CC DNA optimized for TLR9 of the first species; (ii) identifying key amino
 CC acids in human TLR9 which confer specificity for CpG DNA optimized for
 CC human TLR9; (iii) identify a TLR9 ligand; and (iv) identify species-
 CC specific CpG-motif preference of the isolated polypeptide. The screening
 CC method to identify species-specific CpG-motif preference of the isolated
 CC polypeptide comprises: contacting an isolated polypeptide with a CpG DNA
 CC comprising a hexamer sequence consisting of GACGTT, AACGTT, CACGTT,
 CC TACGTT, GGC GTT, GCC GTT, GTC GTT, GAT GTT, GAAGTT, GAG GTT, GACATT, GACCTT,
 CC GACTTT, GACGCT, GACGAT, GACGGT, GACGTC, GACGTA and GACGTG; measuring a
 CC signal in response to the contacting; and identifying a species-specific
 CC CpG-motif preference when the signal in response to the contacting is
 CC consistent with TLR9 signaling. The signal comprises expression of a
 CC reporter gene responsive to TLR/IL-1R signal transduction pathway. The
 CC reporter gene is operatively linked to a promoter sensitive to NF-KB. The
 CC CpG DNA is an oligodeoxynucleotide having a sequence consisting of
 CC sequences selected from ADM72319- ADM72337. The polypeptide is useful for
 CC identifying key amino acids in a TLR9 of a first species which confer
 CC specificity for CpG DNA optimized for TLR9 of the first species. The
 CC present sequence represents a porcine TLR9 polypeptide
 XX
 SQ Sequence 1030 AA;

Alignment Scores:

Length:	1030		
Score:	5400.00	Matches:	1026
Percent Similarity:	99.6%	Conservative:	0
Best Local Similarity:	99.6%	Mismatches:	4
Query Match:	86.4%	Indels:	0
DB:	1	Gaps:	0

US-10-561-022-1 (1-3329) x ADM72285 (1-1030)

Qy	55	ATGGGCCCCCGCTGCACCCTGCACCCCTTTCTCTCTGGTGACGGTGACACGCGTGGCT	114
Db	1	MetGlyProArgCysThrLeuHisProLeuSerLeuLeuValGlnValThrAlaLeuAla	20
Qy	115	GCGACTCTGGCCCAAGGCGAGGCTGCCTGCCTTCTGCGCTGTGAGCTCCAGCCCCACGGC	174
Db	21	AlaAlaLeuAlaGlnGlyArgLeuProAlaPheLeuProCysGluLeuGlnProHisGly	40
Qy	175	CTGGTGAATGCAACTGGCTCTTCTCTGAAGTCCGTGCCCCACTTCTCGGCGGCAGCGCCC	234
Db	41	LeuValAsnCysAsnTrpLeuPheLeuLysSerValProHisPheSerAlaAlaAlaPro	60
Qy	235	CGGGCCACGTCACCGCCTCTCTTACTCTCCAACCGCATCCACCCTTGCACGACTCT	294
Db	61	ArgAlaAsnValThrSerLeuSerLeuLeuSerAsnArgIleHisHisLeuHisAspSer	80
Qy	295	GACTTCGTCCACTGTCCAGCCTACGAACTCTCAACCTCAAGTGGAACTGCCGCGCGCT	354
Db	81	AspPheValHisLeuSerSerLeuArgThrLeuAsnLeuLysTrpAsnCysProProAla	100
Qy	355	GGCCTCAGCCCCATGCACTTCCCTGCCACATGACCATCAGAGCCCAACACCTTCTCGGCC	414
Db	101	GlyLeuSerProMetHisPheProCysHisMetThrIleGluProAsnThrPheLeuAla	120
Qy	415	GTGCCACCCCTGGAGGAGCTGAACCTGAGCTACAACAGCATCACGACCTGGCTGCCCTG	474
Db	121	ValProThrLeuGluGluLeuAsnLeuSerTyrAsnSerIleThrThrValProAlaLeu	140
Qy	475	CCCGACTCCCTCGTGTCCCTGTGCTGAGCGCGACCAACATCCTGGTGTAGACCCACCC	534
Db	141	ProAspSerLeuValSerLeuSerLeuSerArgThrAsnIleLeuValLeuAspProThr	160
Qy	535	CACCTCACTGGCCTACATGCCCTGCGCTACCTGTACATGGATGGCACTGCTACTACAAG	594
Db	161	HisLeuThrGlyLeuHisAlaLeuArgTyrLeuTyrMetAspGlyAsnCysTyrTyrLys	180
Qy	595	AACCCCTGCCAGGGGGCGCTGGAGGTGGTGCCGGGTGCCCTCCTCGCCCTGGGCAACCTC	654
Db	181	AsnProCysGlnGlyAlaLeuGluValValProGlyAlaLeuLeuGlyLeuGlyAsnLeu	200
Qy	655	ACACATCTCTCACTCAAGTACAACAATCTCACGGAGGTGCCCGCAGCTGCCCCCAGC	714
Db	201	ThrHisLeuSerLeuLysTyrAsnAsnLeuThrGluValProArgSerLeuProProSer	220
Qy	715	CTGGAGACCCTGCTGTGTCTTACAACCACATTGTACCCCTGACGCTGAGGACCTGGCC	774
Db	221	LeuGluThrLeuLeuLeuSerTyrAsnHisIleValThrLeuThrProGluAspLeuAla	240
Qy	775	AATCTGACTGCCCTGCCGTGCTTGATGTGGGGGGAATGCCGCGCTGTGACCATGCC	834

Db	241	AsnLeuThrAlaLeuArgValLeuAspValGlyGlyAsnCysArgArgCysAspHisAla	260
Qy	835	CGCAACCCCTGCAGGAGTGCCCAAAGGACCACCCCAAGCTGCACCTCTGACACCTTCAGC	894
Db	261	ArgAsnProCysArgGluCysProLysAspHisProLysLeuHisSerAspThrPheSer	280
Qy	895	CACCTGAGCCGCTCGAAGGCCTGGTGTGAAAGACAGTTCTCTCTACAACCTGGACGCC	954
Db	281	HisLeuSerArgLeuGluGlyLeuValLeuLysAspSerSerLeuTyrAsnLeuAspThr	300
Qy	955	AGGTGGTTCGAGGCCCTGGACAGGCTCCAAGTGCTGGACCTGAGTGAGAAGCTTCCTCTAC	1014
Db	301	ArgTrpPheArgGlyLeuAspArgLeuGlnValLeuAspLeuSerGluAsnPheLeuTyr	320
Qy	1015	GACTGCATCACCAAGACCACGGCCTTCCAGGGCCTGGCCCGACTGCGCAAGCTCAACCTG	1074
Db	321	AspCysIleThrLysThrThrAlaPheGlnGlyLeuAlaArgLeuArgSerLeuAsnLeu	340
Qy	1075	TCCTTCAATTACCACAAGAAGGTGTCCTTTGGCCACCTGCACCTGGCACCTCCTTTGGG	1134
Db	341	SerPheAsnTyrHisLysLysValSerPheAlaHisLeuHisLeuAlaProSerPheGly	360
Qy	1135	CACCTCCGGTCCCTGAAGGAGCTGGACATGCATGGCATCTTCTCCGCTCGCTCAGTGAG	1194
Db	361	HisLeuArgSerLeuLysGluLeuAspMetHisGlyIlePhePheArgSerLeuSerGlu	380
Qy	1195	ACCACGCTCCAACCTCTGGTCCAACCTGCCTATGCTCCAGACCCCTGCCTCGAGATGAAC	1254
Db	381	ThrThrLeuGlnProLeuValGlnLeuProMetLeuGlnThrLeuArgLeuGlnMetAsn	400
Qy	1255	TTCATTAAACAGGCCAGCTCAGCATCTTTGGGGCCTTCCCTGGCCTGCTGTACGTGGAC	1314
Db	401	PheIleAsnGlnAlaGlnLeuSerIlePheGlyAlaPheProGlyLeuLeuTyrValAsp	420
Qy	1315	CTATCGGACAACCGCATCAGCGAGCTGCAAGGCCAGTGGCCATTACTAGGGAGGTGGAT	1374
Db	421	LeuSerAspAsnArgIleSerGlyAlaAlaArgProValAlaIleThrArgGluValAsp	440
Qy	1375	GGTAGGGAGAGGGTCTGGCTGCCTTCCAGGAACCTCGCTCCACGTCCACTGGACACTCTC	1434
Db	441	GlyArgGluArgValTrpLeuProSerArgAsnLeuAlaProArgProLeuAspThrLeu	460
Qy	1435	CGCTCAGAGGACTTCATGCCAACTGCAAGGCCTTCAGCTTCACCTTGGACCTGTCTCGG	1494
Db	461	ArgSerGluAspPheMetProAsnCysLysAlaPheSerPheThrLeuAspLeuSerArg	480
Qy	1495	AACAACCTGGTGACATCCAGTCGGAGATGTTTGCTCGCTCTCACGCCCTCGAGTGCCTG	1554
Db	481	AsnAsnLeuValThrIleGlnSerGluMetPheAlaArgLeuSerArgLeuGluCysLeu	500
Qy	1555	CGTCTGAGCCACAACAGCATCTCCAGGCGGTCAATGGCTCTCAGTTTGTCGCGGTGACC	1614
Db	501	ArgLeuSerHisAsnSerIleSerGlnAlaValAsnGlySerGlnPheValProLeuThr	520
Qy	1615	AGCCTCGCGGTGCTGGACCTGTCCCAACAAGCTGGACCTGTATCACGGGCGCTCGTTC	1674
Db	521	SerLeuArgValLeuAspLeuSerHisAsnLysLeuAspLeuTyrHisGlyArgSerPhe	540
Qy	1675	ACGGAGCTGCCGCGCTGGAAGCACTGGACCTCAGCTACAACAGCCAGCCCTTACCATG	1734
Db	541	ThrGluLeuProArgLeuGluAlaLeuAspLeuSerTyrAsnSerGlnProPheThrMet	560

Qy	1735	CAGGGTGTGGGCCCAACCTCAGCTTCGTGGCCAGCTGCCGCCCTGCCTACCTCAGC	1794
Db	561	GlnGlyValGlyHisAsnLeuSerPheValAlaGlnLeuProAlaLeuArgTyrLeuSer	580
Qy	1795	CTGGCGCACAATGACATCCATAGCCGAGTGTCCCAGCAGCTCTGTAGCGCCTCACTGTGC	1854
Db	581	LeuAlaHisAsnAspIleHisSerArgValSerGlnGlnLeuCysSerAlaSerLeuCys	600
Qy	1855	GCCCTGGACTTTAGCGGCAACGATCTGAGCCGGATGTGGGCTGAGGGAGACCTCTATCTC	1914
Db	601	AlaLeuAspPheSerGlyAsnAspLeuSerArgMetTrpAlaGluGlyAspLeuTyrLeu	620
Qy	1915	CGCTTCTTCCAAGGCCTAAGAAGCCTAGTCTGGCTGGACCTGTCCAGAACACCTGCAC	1974
Db	621	ArgPhePheGlnGlyLeuArgSerLeuValTrpLeuAspLeuSerGlnAsnHisLeuHis	640
Qy	1975	ACCCTCCTGCCAGTGGCCCTGGACAACCTCCCCAAAAGCCTGAAGCATCTGCATCTCCGT	2034
Db	641	ThrLeuLeuProArgAlaLeuAspAsnLeuProLysSerLeuLysHisLeuHisLeuArg	660
Qy	2035	GACAATAACCTGGCCTTCTTCAACTGGAGCAGCCTGACCTCCTGCCCAAGCTGGAAACC	2094
Db	661	AspAsnAsnLeuAlaPhePheAsnTrpSerSerLeuThrLeuLeuProLysLeuGluThr	680
Qy	2095	CTGGACTTGGCTGGAAACCAGCTGAAGGCCCTAAGCAATGGCAGCCTGCCACTTGGCACC	2154
Db	681	LeuAspLeuAlaGlyAsnGlnLeuLysAlaLeuSerAsnGlySerLeuProSerGlyThr	700
Qy	2155	CAGCTCGGGAGGCTGGACCTCAGTGGCAACAGCATCGGCTTTGTGAACCTGGCTTCTTT	2214
Db	701	GlnLeuArgArgLeuAspLeuSerGlyAsnSerIleGlyPheValAsnProGlyPhePhe	720
Qy	2215	GCCCTGGCCAAGCAGTTAGAAGAGCTCAACCTCAGCGCCAATGCCCTCAAGACAGTGGAG	2274
Db	721	AlaLeuAlaLysGlnLeuGluGluLeuAsnLeuSerAlaAsnAlaLeuLysThrValGlu	740
Qy	2275	CCCTCTGGTTTGGCTCGATGGTGGGCAACCTGAAAGTCTAGACGTGAGCGCCAACCT	2334
Db	741	ProSerTrpPheGlySerMetValGlyAsnLeuLysValLeuAspValSerAlaAsnPro	760
Qy	2335	CTGCACTGCGCTGTGGGGCGACCTTCGTGGGCTTCCTGCTGGAGGTACAGGCTGCCGTG	2394
Db	761	LeuHisCysAlaCysGlyAlaThrPheValGlyPheLeuLeuGluValGlnAlaAlaVal	780
Qy	2395	CCTGGGCTGCCAGCCGCGCTCAAGTGTGGCAGTCCGGGGCAGCTCCAGGGCCATAGCATC	2454
Db	781	ProGlyLeuProSerArgValLysCysGlySerProGlyGlnLeuGlnGlyHisSerIle	800
Qy	2455	TTTGCGCAAGACCTGCGCCTCTGCCTGGATGAGACCTCTCTGTGGAAGTGTTTTGGCATC	2514
Db	801	PheAlaGlnAspLeuArgLeuCysLeuAspGluThrLeuSerTrpAsnCysPheGlyIle	820
Qy	2515	TCGCTGCTGGCCATGGCCCTGGGCTGGTTGTGCCCATGCTGCACCACCTCTGCGGCTGG	2574
Db	821	SerLeuLeuAlaMetAlaLeuGlyLeuValValProMetLeuHisHisLeuCysGlyTrp	840
Qy	2575	GACCTCTGGTACTGCTTCCACCTGTGCTGGCCTGGCTGCCACCAGGGGAGCGGCGG	2634
Db	841	AspLeuTrpTyrCysPheHisLeuCysLeuAlaTrpLeuProHisArgGlyGlnArgArg	860

Qy	2635	GGCGCAGACGCCCTGTTCTATGATGCCTTCGTGGTCTTTGACAAAGCTCAGAGTGCTGTG	2694
Db	861	GlyAlaAspAlaLeuPheTyrAspAlaPheValValPheAspLysAlaGlnSerAlaVal	880
Qy	2695	GCCGACTGGGTGTACAACGAGCTGCGGGTGCAGCTGGAGGAGCGCCGTGGGCGCCGCGCA	2754
Db	881	AlaAspTrpValTyrAsnGluLeuArgValGlnLeuGluGluArgArgGlyArgArgAla	900
Qy	2755	CTGCGCCTGTGCCTGGAGGAGCGAGACTGGTTACCTGGCAAGACGCTCTTCGAGAACCTG	2814
Db	901	LeuArgLeuCysLeuGluGluArgAspTrpLeuProGlyLysThrLeuPheGluAsnLeu	920
Qy	2815	TGGGCCTCAGTCTACAGCAGCCGCAAGACCCTGTTTGTGCTGGCCACACGGACCGTGTC	2874
Db	921	TrpAlaSerValTyrSerSerArgLysThrLeuPheValLeuAlaHisThrAspArgVal	940
Qy	2875	AGCGGCCTCTTGCGTGCCAGTTTCTGTGCTGGCCACGAGCGCTGTGGAGGACCGAAG	2934
Db	941	SerGlyLeuLeuArgAlaSerPheLeuLeuAlaGlnGlnArgLeuLeuGluAspArgLys	960
Qy	2935	GACGTTGTAGTGCTGGTGATCCTGCGCCCCGATGCCTACCGCTCCCCTACGTGCGGGCTG	2994
Db	961	AspValValValLeuValIleLeuArgProAspAlaTyrArgSerArgTyrValArgLeu	980
Qy	2995	CGCCAGCGCCTCTGCCGCCAGAGTGTCCTCTCTGGCCCCACAGCCCCGTGGGCAGGGC	3054
Db	981	ArgGlnArgLeuCysArgGlnSerValLeuLeuTrpProHisGlnProArgGlyGlnGly	1000
Qy	3055	AGCTTCTGGGCCCAGCTGGGCACAGCCCTGACCAGGGACAACCGCCACTTCTATAACCGG	3114
Db	1001	SerPheTrpAlaGlnLeuGlyThrAlaLeuThrArgAspAsnHisHisPheTyrAsnArg	1020
Qy	3115	AACTTCTGCGGGGCCCCACGACAGCCGAA	3144
Db	1021	AsnPheCysArgGlyProThrThrAlaGlu	1030